GenCore version 4.5


OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:20 ; Search time 13.33 Seconds
(without alignments)
97.147 Million cell updates/sec

Title: US-09-497-997B-1
Perfect score: 98
Sequence: 1 TRQKYNKRAMDYWGQGT 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 65 | 66.3 | 122 | 2 | E27888 | Ig heavy chain V r |
| 2 | 64.5 | 65.8 | 139 | 2 | PS0024 | Ig heavy chain pre |
| 3 | 63 | 64.3 | 120 | 2 | S03484 | Ig heavy chain V-D |
| 4 | 62 | 63.3 | 119 | 2 | S09955 | Ig heavy chain V-D |
| 5 | 62 | 63.3 | 138 | 2 | E32513 | Ig heavy chain pre |
| 6 | 61 | 62.2 | 99 | 2 | S26326 | Ig heavy chain V r |
| 7 | 61 | 62.2 | 120 | 2 | E45722 | anti-glycoprotein |
| 8 | 60.5 | 61.7 | 122 | 2 | S20642 | Ig heavy chain V r |
| 9 | 60 | 61.2 | 104 | 2 | S26466 | Ig heavy chain V r |
| 10 | 60 | 61.2 | 117 | 2 | S38563 | Ig heavy chain V r |
| 11 | 59.5 | 60.7 | 122 | 2 | S20643 | Ig heavy chain V r |
| 12 | 59 | 60.2 | 101 | 2 | D24672 | Ig heavy chain V r |
| 13 | 59 | 60.2 | 107 | 2 | S26320 | Ig heavy chain V r |
| 14 | 59 | 60.2 | 109 | 2 | S26318 | Ig heavy chain V r |
| 15 | 59 | 60.2 | 111 | 2 | S26324 | Ig heavy chain V r |
| 16 | 59 | 60.2 | 117 | 2 | B27563 | Ig heavy chain V r |
| 17 | 59 | 60.2 | 118 | 2 | S20641 | Ig heavy chain V r |
| 18 | 59 | 60.2 | 136 | 2 | S04576 | Ig heavy chain pre |
| 19 | 59 | 60.2 | 139 | 2 | A27609 | Ig heavy chain pre |
| 20 | 58.5 | 59.7 | 123 | 2 | S20646 | Ig heavy chain V r |
| 21 | 58 | 59.2 | 119 | 2 | F27888 | Ig heavy chain V r |
| 22 | 57.5 | 58.7 | 113 | 2 | S26468 | Ig heavy chain V r |
| 23 | 57.5 | 58.7 | 120 | 2 | S41394 | Ig heavy chain V r |
| 24 | 57 | 58.2 | 30 | 2 | PL0092 | Ig heavy chain V r |
| 25 | 57 | 58.2 | 110 | 2 | S26323 | Ig heavy chain V r |
| 26 | 57 | 58.2 | 111 | 2 | PH1643 | Ig heavy chain V r |
| 27 | 57 | 58.2 | 114 | 2 | PL0256 | Ig heavy chain V r |
| 28 | 57 | 58.2 | 125 | 2 | PH0100 | Ig heavy chain V r |
| 29 | 57 | 58.2 | 149 | 2 | S30752 | Ig heavy chain pre |
| 30 | 57 | 58.2 | 246 | 2 | S38950 | Ig gamma chain - m |
| 31 | 57 | 58.2 | 446 | 2 | S40295 | Ig gamma-2a chain |
| 32 | 56.5 | 57.7 | 117 | 2 | PL0237 | Ig heavy chain V r |
| 33 | 56.5 | 57.7 | 117 | 2 | PL0234 | Ig heavy chain V r |
| 34 | 56 | 57.1 | 119 | 2 | D30540 | Ig heavy chain V r |
| 35 | 56 | 57.1 | 120 | 2 | S55536 | Ig heavy chain V r |
| 36 | 56 | 57.1 | 120 | 2 | S55539 | Ig heavy chain V r |
| 37 | 56 | 57.1 | 120 | 2 | S55537 | Ig heavy chain V r |
| 38 | 56 | 57.1 | 120 | 2 | PD0008 | Ig heavy chain V r |
| 39 | 56 | 57.1 | 122 | 2 | S24287 | Ig heavy chain V r |
| 40 | 56 | 57.1 | 123 | 2 | S32186 | Ig heavy chain V r |
| 41 | 56 | 57.1 | 136 | 1 | G1MS21 | Ig heavy chain pre |
| 42 | 56 | 57.1 | 151 | 2 | PL0011 | Ig heavy chain pre |
| 43 | 56 | 57.1 | 254 | 2 | B31790 | Ig heavy chain V r |
| 44 | 55.5 | 56.6 | 126 | 2 | S31930 | Ig gamma chain pre |
| 45 | 55 | 56.1 | 10 | 2 | F33932 | Ig mu chain J regi |

ALIGNMENTS

RESULT 1
E27888
Ig heavy chain V region (H35-C6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: E27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to
A;Reference number: A91043; MUID:86300658
A;Accession: E27888
A;Molecule type: DNA
A;Residues: 1-122 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza viru
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 65; DB 2; Length 122;
Best Local Similarity 61.9%; Pred. No. 0.0057;
Matches 13; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

```
Qy       1 TRQ----KYNKRAMDYWGQGT 17
             |||    :|:  |||||||||
Db      97 TRQGEGYRYDDYAMDYWGQGT 117
```

RESULT 2
PS0024
Ig heavy chain precursor V region (6A4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C;Accession: PS0024
R;Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A;Title: Cloning and characterization of cDNAs coding for the heavy and light chains
A;Reference number: PS0023; MUID:89232725
A;Accession: PS0024
A;Molecule type: mRNA
A;Residues: 1-139 <MAR>
A;Experimental source: strain BALB/c
C;Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomon
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F;34-117/Domain: immunoglobulin homology <IMM>
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predic

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  Query Match             65.8%;  Score 64.5;  DB 2;  Length 139;
  Best Local Similarity   72.2%;  Pred. No. 0.0076;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       1 TRQKYN-KRAMDYWGQGT 17
           ||  || : |||||||||
Db     116 TRSYYNYEGAMDYWGQGT 133


RESULT   3
S03484
Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hy[redacted]variable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             64.3%;  Score 63;  DB 2;  Length 120;
  Best Local Similarity   64.7%;  Pred. No. 0.011;
  Matches   11;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           ||  : : |||||||||
Db      97 TRGWFRRDAMDYWGQGT 113


RESULT   4
S09955
Ig heavy chain V-D-J region (103-7E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Accession: S09955
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: S09955; MUID:90269328
A;Accession: S09955
A;Molecule type: mRNA
A;Residues: 1-119 <REI>
A;Cross-references: EMBL:X51843; NID:g55242; PIDN:CAA36136.1; PID:g930211
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             63.3%;  Score 62;  DB 2;  Length 119;
  Best Local Similarity   70.6%;  Pred. No. 0.016;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
             |||     |||||||||
Db      97 TRQSGTWDAMDYWGQGT 113


RESULT   5
E32513
Ig heavy chain precursor V region (MRL22) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C;Accession: E32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization a
A;Reference number: A94689; MUID:88331394
A;Accession: E32513
A;Molecule type: DNA
A;Residues: 1-138 <KOF>
A;Cross-references: GB:M20835; NID:g196945; PIDN:AAA38847.1; PID:g196946
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>


  Query Match             63.3%;  Score 62;  DB 2;  Length 138;
  Best Local Similarity   68.8%;  Pred. No. 0.018;
  Matches   11;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 RQKYNKRAMDYWGQGT 17
           |: |   |||||||||
Db     117 RRLYRYYAMDYWGQGT 132


RESULT   6
S26326
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C;Accession: S26326
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26326
A;Molecule type: mRNA
A;Residues: 1-99 <STA>
A;Cross-references: EMBL:X59174
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin


  Query Match             62.2%;  Score 61;  DB 2;  Length 99;
  Best Local Similarity   68.8%;  Pred. No. 0.019;
  Matches   11;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 RQKYNKRAMDYWGQGT 17
           |: |   |||||||||
Db      78 REGYYYYAMDYWGQGT 93


RESULT   7
E45722
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 5) - mouse (
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: E45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A;Reference number: A45722; MUID:93100833
A;Accession: E45722
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-120 <SIM>
```

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A;Note: sequence extracted from NCBI backbone (NCBIP:120593)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;15-99/Domain: immunoglobulin homology <IMM>


  Query Match             62.2%;  Score 61;  DB 2;  Length 120;
  Best Local Similarity   58.8%;  Pred. No. 0.023;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 TRQKYNKRAMDYWGQGT 17
          ||: .:   :|||||||||
Db     98 TRRGFRDYSMDYWGQGT 114


RESULT   8
S20642
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20642
R;[redacted]an, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Accession: S20642
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-122 <LOS>
A;Cross-references: EMBL:X64997; NID:g52604; PIDN:CAA46130.1; PID:g52605
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>


  Query Match             61.7%;  Score 60.5;  DB 2;  Length 122;
  Best Local Similarity   66.7%;  Pred. No. 0.028;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    1;  Gaps    1;

Qy      1 TRQKYNKR-AMDYWGQGT 17
          ||:  ::| |||||||||
Db     99 TRKAASRRGAMDYWGQGT 116


RESULT   9
S26466
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;[redacted]te: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;[redacted]ession: S26466
R;[redacted]valer, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S26466
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <KAV>
A;Cross-references: EMBL:X59116; NID:g51933; PIDN:CAA41842.1; PID:g51934
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>


  Query Match             61.2%;  Score 60;  DB 2;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 0.029;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      8 RAMDYWGQGT 17
          ||||||||||
Db     90 RAMDYWGQGT 99


RESULT  10
S38563
Ig heavy chain V region (ASWS1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38563
R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2
A;Reference number: S38559
A;Accession: S38563
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MON>
A;Cross-references: EMBL:X75099; NID:g414151; PIDN:CAA52990.1; PID:g414152
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>


  Query Match             61.2%;  Score 60;  DB 2;  Length 117;
  Best Local Similarity   68.8%;  Pred. No. 0.032;
  Matches   11;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      2 RQKYNKRAMDYWGQGT 17
          |  |   |||||||||
Db     97 RDGYYDYAMDYWGQGT 112


RESULT  11
S20643
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20643
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice re
A;Reference number: S20639
A;Accession: S20643
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-122 <LOS>
A;Cross-references: EMBL:X64998; NID:g52606; PIDN:CAA46131.1; PID:g52607
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             60.7%;  Score 59.5;  DB 2;  Length 122;
  Best Local Similarity   63.2%;  Pred. No. 0.04;
  Matches   12;  Conservative    2;  Mismatches    2;  Indels    3;  Gaps    1;

Qy      2 RQKYNKR---AMDYWGQGT 17
          |: |: |   |||||||||
Db     99 REYYDLRRGHAMDYWGQGT 117


RESULT  12
D24672
Ig heavy chain V region (VGAM3-8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C;Accession: D24672
R;Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A;Reference number: A91022; MUID:86055722
A;Accession: D24672
A;Molecule type: DNA
A;Residues: 1-101 <WIN>
A;Cross-references: GB:X03301; NID:g51757; PIDN:CAA27040.1; PID:g773215
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
```

```
  Query Match           60.2%;  Score 59;  DB 2;  Length 101;
  Best Local Similarity  76.9%;  Pred. No. 0.04;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 YNKRAMDYWGQGT 17
           |:  |||||||||
Db      83 YDYYAMDYWGQGT 95


RESULT  13
S26320
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S26320
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421
A;Accession: S26320
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
A;Cross-references: EMBL:X59206
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>


  Query Match           60.2%;  Score 59;  DB 2;  Length 107;
  Best Local Similarity  76.9%;  Pred. No. 0.042;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 YNKRAMDYWGQGT 17
           |   |||||||||
Db      90 YRDYAMDYWGQGT 102


RESULT  14
S26318
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26318
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421
A;Accession: S26318
A;Molecule type: mRNA
A;Residues: 1-109 <STA>
A;Cross-references: EMBL:X59200
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>


  Query Match           60.2%;  Score 59;  DB 2;  Length 109;
  Best Local Similarity  76.9%;  Pred. No. 0.043;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 YNKRAMDYWGQGT 17
           | : |||||||||
Db      91 YFRYAMDYWGQGT 103


RESULT  15
S26324
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26324
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26324
A;Molecule type: mRNA
A;Residues: 1-111 <STA>
A;Cross-references: EMBL:X59178
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-88/Domain: immunoglobulin homology <IMM>


  Query Match           60.2%;  Score 59;  DB 2;  Length 111;
  Best Local Similarity  83.3%;  Pred. No. 0.043;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       6 NKRAMDYWGQGT 17
           |  |||||||||
Db      94 NYEAMDYWGQGT 105


Search completed: June 27, 2001, 11:28:54
Job time: 34 sec
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GenCore version 4.5


OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:20 ; Search time 19.1 Seconds
(without alignments)
53.959 Million cell updates/sec

Title: US-09-497-997B-1
Perfect score: 98
Sequence: 1 TRQKYNKRAMDYWGQGT 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601:*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
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19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 98 | 100.0 | 17 | 20 | AAW99559 | Immunoglobulin IgG |
| 2 | 88 | 89.8 | 17 | 20 | AAW99561 | Immunoglobulin IgG |
| 3 | 83.5 | 85.2 | 18 | 20 | AAW99562 | Immunoglobulin IgG |
| 4 | 64.5 | 65.8 | 159 | 10 | AAP93079 | Heavy chain of mon |
| 5 | 64 | 65.3 | 140 | 18 | AAW21841 | Heavy chain variab |
| 6 | 62 | 63.3 | 119 | 16 | AAR74940 | Immunoglobulin hea |
| 7 | 62 | 63.3 | 119 | 18 | AAW01578 | Lead binding MAb 8 |
| 8 | 62 | 63.3 | 133 | 16 | AAR74960 | Anti-idiotype anti |
| 9 | 62 | 63.3 | 135 | 16 | AAR74961 | Anti-idiotype anti |
| 10 | 62 | 63.3 | 143 | 21 | AAY43867 | Heavy chain (VH) g |
| 11 | 62 | 63.3 | 144 | 21 | AAY43857 | Heavy chain framew |
| 12 | 62 | 63.3 | 436 | 21 | AAY91026 | Apoptobody3sc fusi |
| 13 | 61 | 62.2 | 119 | 13 | AAR25730 | Humanised VH regio |
| 14 | 61 | 62.2 | 119 | 22 | AAB69679 | Murine CMV5 antibo |
| 15 | 61 | 62.2 | 119 | 22 | AAB69680 | Humanised CMV5 ant |
| 16 | 61 | 62.2 | 119 | 22 | AAB69692 | Human Wol antibody |
| 17 | 61 | 62.2 | 138 | 17 | AAW03722 | Anti-human gp39 MA |
| 18 | 61 | 62.2 | 138 | 22 | AAB69688 | Murine CMV5 antibo |
| 19 | 61 | 62.2 | 139 | 13 | AAR27053 | Anti-CEA specific |
| 20 | 61 | 62.2 | 139 | 14 | AAR30480 | hCEA specific mous |
| 21 | 61 | 62.2 | 141 | 21 | AAY43869 | Heavy chain (VH) g |
| 22 | 61 | 62.2 | 142 | 21 | AAY43868 | Heavy chain (VH) g |
| 23 | 61 | 62.2 | 184 | 17 | AAW03726 | Humanised MAb 39-1 |
| 24 | 60 | 61.2 | 12 | 20 | AAW99560 | Immunoglobulin IgG |
| 25 | 60 | 61.2 | 118 | 16 | AAR79865 | Anti-EGFR antibody |
| 26 | 60 | 61.2 | 119 | 21 | AAY92156 | Murine 15B8 heavy |
| 27 | 60 | 61.2 | 141 | 21 | AAY43859 | Heavy chain framew |
| 28 | 60 | 61.2 | 145 | 21 | AAY43856 | Heavy chain framew |
| 29 | 60 | 61.2 | 147 | 21 | AAY43860 | Heavy chain framew |
| 30 | 59 | 60.2 | 118 | 15 | AAR50323 | MAb NFS2 heavy cha |
| 31 | 59 | 60.2 | 118 | 16 | AAR79242 | Heavy chain variab |
| 32 | 59 | 60.2 | 122 | 15 | AAR50311 | Humanised heavy ch |
| 33 | 59 | 60.2 | 122 | 15 | AAR50312 | Humanised heavy ch |
| 34 | 59 | 60.2 | 122 | 15 | AAR50315 | Humanised heavy ch |
| 35 | 59 | 60.2 | 124 | 18 | AAW01594 | Lead binding MAb 2 |
| 36 | 59 | 60.2 | 240 | 9 | AAP80153 | Binding site. AA |
| 37 | 58 | 59.2 | 115 | 18 | AAW04595 | Anti-DNA antibody |
| 38 | 58 | 59.2 | 116 | 16 | AAR64224 | Anti-(6-4) photopr |
| 39 | 58 | 59.2 | 123 | 16 | AAR81323 | Humanized VLA-4 an |
| 40 | 58 | 59.2 | 123 | 16 | AAR81330 | Mouse anti-VLA-4 a |
| 41 | 58 | 59.2 | 123 | 18 | AAW07438 | Anti-DNA antibody |
| 42 | 58 | 59.2 | 140 | 16 | AAR81327 | Mouse VLA-4 antibo |
| 43 | 58 | 59.2 | 140 | 18 | AAW22410 | Alpha-4 integrin m |
| 44 | 58 | 59.2 | 142 | 16 | AAR81333 | Human VLA-4 reshap |
| 45 | 58 | 59.2 | 142 | 18 | AAW22428 | Humanised alpha-4 |

ALIGNMENTS

RESULT 1
AAW99559
ID AAW99559 standard; peptide; 17 AA.
XX
AC AAW99559;
XX
DT 22-JUN-1999 (first entry)
XX
DE Immunoglobulin IgG2a CDR3-derived peptide #1.
XX
KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN FR2766826-A1.
XX
PD 05-FEB-1999.
XX
PF 04-AUG-1997; 97FR-0009972.
XX
PR 04-AUG-1997; 97FR-0009972.
XX
PA (INSP ) INST PASTEUR.
XX
PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
XX
DR WPI; 1999-156194/14.
XX
PT New polypeptide including sequence from single antibody chain and
PT able to penetrate a cell - used as vector for delivering attached
PT components, e.g. nucleic acid or antigen, to cells, useful in gene
PT therapy and vaccination

XX
PS Example 2; Page 19; 36pp; French.
XX
CC This sequence corresponds to a peptide derived from the complementary
CC determining region 3 (CDR3) of an immunoglobulin IgG2a protein and is
CC used in the production of a polypeptide that (i) comprises a unique or
CC repeated peptide motif; (ii) includes a sequence consisting of one or
CC more different antibody fragments and (iii) can penetrate into cells.
CC The polypeptides are vectors for delivering a substance to cells
CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
CC (gene therapy, or where the substance is an antigen, for vaccination,
CC in which case the polypeptide acts effectively as an adjuvant).
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 98; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TRQKYNKRAMDYWGQGT 17
||||||||||||||||
Db 1 trqkynkramdywgqgt 17

RESULT 2
AAW99561
ID AAW99561 standard; peptide; 17 AA.
XX
AC AAW99561;
XX
DT 22-JUN-1999 (first entry)
XX
DE Immunoglobulin IgG2a CDR3-derived peptide #3.
XX
KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN FR2766826-A1.
XX
PD 05-FEB-1999.
XX
PF 04-AUG-1997; 97FR-0009972.
XX
PR 04-AUG-1997; 97FR-0009972.
XX
PA (INSP ) INST PASTEUR.
XX
PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
XX
DR WPI; 1999-156194/14.
XX
PT New polypeptide including sequence from single antibody chain and
PT able to penetrate a cell - used as vector for delivering attached
PT components, e.g. nucleic acid or antigen, to cells, useful in gene
PT therapy and vaccination
XX
PS Example 2; Page 19; 36pp; French.
XX
CC This sequence corresponds to a peptide derived from the complementary
CC determining region 3 (CDR3) of an immunoglobulin IgG2a protein and is
CC used in the production of a polypeptide that (i) comprises a unique or
CC repeated peptide motif; (ii) includes a sequence consisting of one or
CC more different antibody fragments and (iii) can penetrate into cells.
CC The polypeptides are vectors for delivering a substance to cells
CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
CC (gene therapy, or where the substance is an antigen, for vaccination,
CC in which case the polypeptide acts effectively as an adjuvant).
XX
SQ Sequence 17 AA;

Query Match 89.8%; Score 88; DB 20; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TRQKYNKRAMDYWGQGT 17
||||| || ||||||||
Db 1 trqkygkrgmdywgqgt 17

RESULT 3
AAW99562
ID AAW99562 standard; peptide; 18 AA.
XX
AC AAW99562;
XX
DT 22-JUN-1999 (first entry)
XX
DE Immunoglobulin IgG2a CDR3-derived peptide #4.
XX
KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN FR2766826-A1.
XX
PD 05-FEB-1999.
XX
PF 04-AUG-1997; 97FR-0009972.
XX
PR 04-AUG-1997; 97FR-0009972.
XX
PA (INSP ) INST PASTEUR.
XX
PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
XX
DR WPI; 1999-156194/14.
XX
PT New polypeptide including sequence from single antibody chain and
PT able to penetrate a cell - used as vector for delivering attached
PT components, e.g. nucleic acid or antigen, to cells, useful in gene
PT therapy and vaccination
XX
PS Example 2; Page 19; 36pp; French.
XX
CC This sequence corresponds to a peptide derived from the complementary
CC determining region 3 (CDR3) of an immunoglobulin IgG2a protein and is
CC used in the production of a polypeptide that (i) comprises a unique or
CC repeated peptide motif; (ii) includes a sequence consisting of one or
CC more different antibody fragments and (iii) can penetrate into cells.
CC The polypeptides are vectors for delivering a substance to cells
CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
CC (gene therapy, or where the substance is an antigen, for vaccination,
CC in which case the polypeptide acts effectively as an adjuvant).
XX
SQ Sequence 18 AA;

Query Match 85.2%; Score 83.5; DB 20; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 TRQKYN-KRAMDYWGQGT 17
|||||| || ||||||||
Db 1 trqkynkkrgmdywgqgt 18

RESULT 4
AAP93079
ID AAP93079 standard; peptide; 159 AA.

XX
AC AAP93079;
XX
DT 15-MAR-1990 (first entry)
XX
DE Heavy chain of monoclonal antibody 6A4.
XX
KW Monoclonal antibody 6A4; heavy chain; Pseudomonas aeruginosa; OMP-1.
XX
PN EP338395-A.
XX
PD 25-OCT-1989.
XX
PF 12-APR-1989; 89EP-0106463.
XX
PR 19-APR-1988; 88DE-3813023.
XX
PA (BEHW ) BEHRINGWERKE.
XX
PI Domdey H, Marget M, von Specht BU;
XX
DR WPI; 1989-310861/43.
DR N-PSDB; AAN91645.
XX
PT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
PT variable antibody regions.
XX
PS Claim 1; page 6; 7pp; german.
XX
CC The peptide is encoded by the heavy chain of monoclonal antibody 6A4.
CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of
CC P.aeruginosa. It is used for therapy and diagnosis of infection, and as
CC a carrier for drugs. The antibody is IgG2a subclass.
XX
SQ Sequence 159 AA;

Query Match 65.8%; Score 64.5; DB 10; Length 159;
Best Local Similarity 72.2%; Pred. No. 0.03;
Matches 13; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 TRQKYN-KRAMDYWGQGT 17
|| || : |||||||||
Db 116 trsyynyegamdywgqgt 133

RESULT 5
AAW21841
ID AAW21841 standard; Protein; 140 AA.
XX
AC AAW21841;
XX
DT 18-DEC-1997 (first entry)
XX
DE Heavy chain variable region of KM1257 antibody.
XX
KW Complementarity determining region; CDR; heavy chain; treatment;
KW variable region; murine; mouse; human; interleukin 5; IL-5;
KW receptor; alpha chain; monoclonal antibody; hybridoma; detection;
KW assay; diagnosis; allergic respiratory disease;
KW chronic bronchitis.
XX
OS Mus spp.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig_peptide
FT Peptide 20..140
FT /label= mat_peptide
FT Region 50..54
FT /label= complementarity_determining_region_1
FT Region 69..85
FT /label= complementarity_determining_region_2
FT Region 118..129
FT /label= complementarity_determining_region_3
XX
PN WO9710354-A1.
XX
PD 20-MAR-1997.
XX
PF 11-SEP-1996; 96WO-JP02588.
XX
PR 11-SEP-1995; 95JP-0232384.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Anazawa H, Furuya A, Hanai N, Iida A, Koike M;
PI Nakamura K, Takatsu K;
XX
DR WPI; 1997-202249/18.
DR N-PSDB; AAT73608.
XX
PT Antibody against alpha-chain of human interleukin 5 receptor -
PT useful for diagnosis and treatment of respiratory allergic diseases,
PT e.g. chronic bronchitis
XX
PS Example 2; Pages 116-117; 238pp; Japanese.
XX
CC The present sequence is the heavy chain variable region of the
CC murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha)
CC monoclonal antibody (MAb) KM1257. KM1257 is produced by the hybridoma
CC FERM BP-5133, which was prepared by immunising Balb/c mice with
CC hIL-5R alpha, fusing spleen cells obtained from the mice with mouse
CC myeloma P3-U1 cells and screening the resultant hybridomas. The MAb
CC can be used to detect or assay for hIL-5R alpha and cells
CC expressing it on their surface, especially to diagnose allergic
CC respiratory diseases, e.g. chronic bronchitis. It can also be used
CC to treat such diseases.
XX
SQ Sequence 140 AA;

Query Match 65.3%; Score 64; DB 18; Length 140;
Best Local Similarity 91.7%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 NKRAMDYWGQGT 17
| ||||||||||
Db 123 nyramdywgqgt 134

RESULT 6
AAR74940
ID AAR74940 standard; peptide; 119 AA.
XX
AC AAR74940;
XX
DT 19-JAN-1996 (first entry)
XX
DE Immunoglobulin heavy chain of anti-idiotype antibody against human
DE anticancer antibody.
XX
KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..66
FT /label= CDR2
FT Region 99..108
FT /label= CDR3
XX
PN JP07101999-A.

```
XX
PD   18-APR-1995.
XX
PF   06-OCT-1993;   93JP-0272950.
XX
PR   06-OCT-1993;   93JP-0272950.
XX
PA   (HAGI/) HAGIWARA Y.
XX
DR   WPI; 1995-182987/24.
XX
PT   Novel anti-idiotype antibody against an human anticancer monoclonal
PT   antibody  - and DNA sequences encoding the antibody, useful in
PT   pharmacology, medicine and biochemical fields.
XX
PS   Claim 2; Page 2; 28pp; Japanese.
XX
CC   AAR74940-R74943 are possible heavy chains of a new anti-idiotype
CC   antibody against a human anticancer monoconal antibody.This antibody
CC   contains in its heavy chain 3 complemetarity determining regions CDR1
CC   (AAR74929-R74931) CDR2 (AAR74932-R794935) and CDR3 (AAR74936-R74939),
CC   this is also true of the light chain which has its own CDR1
CC   (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3
CC   (AAR74950-R74954). The antibody and DNA encoding it are useful in
CC   pharmacological, medical and biochemical fields.
XX
SQ   Sequence   119 AA;


  Query Match             63.3%;  Score 62;  DB 16;  Length 119;
  Best Local Similarity   52.9%;  Pred. No. 0.053;
  Matches    9;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           |:::|:   :|||||||
Db      97 tkeeydydtldywgqgt 113


RESULT   7
AAW01578
ID   AAW01578 standard; Protein; 119 AA.
XX
AC   AAW01578;
XX
DT   22-AUG-1997  (first entry)
XX
DE   Lead binding MAb 8E7 heavy chain variable region.
XX
KW   Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW   pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW   heavy metal.
XX
OS   Mus musculus.
XX
PN   WO9639518-A1.
XX
PD   12-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US09258.
XX
PR   10-OCT-1995;   95US-0541373.
PR   05-JUN-1995;   95US-0462798.
XX
PA   (BION-) BIONEBRASKA INC.
XX
PI   Lopez O,  Murray PJ,  Wylie DE;
XX
DR   WPI; 1997-043140/04.
DR   N-PSDB; AAT58252.
XX
PT   DNA encoding heavy metal binding polypeptide sequences - used for
PT   detecting, removing, adding or neutralising heavy metals, such as
PT   lead cations
XX
PS   Claim 12; Page 59; 125pp; English.
XX
CC   The present sequence represents the heavy chain variable region for
CC   monoclonal antibody (MAb) 8E7, which immunoreacts with a lead cation.
CC   The sequence was derived from RNA isolated from mouse hybridoma cells.
CC   The protein can be used for binding heavy metals, such as lead cations.
CC   It can be used for detecting, removing, adding or neutralising the
CC   heavy metals in biological and inanimate systems. It can be used in
CC   e.g. aqueous liquid systems, in biological or environmental systems or
CC   in such compositions as perfumes, cosmetics, pharmaceuticals, health
CC   care products, skin treatment products, pesticides, herbicides,
CC   solvents used in the production of semi-conductor and integrated
CC   circuit components and production materials for electronic components.
CC   The products can provide for applications involving minute amounts of
CC   specific heavy metals.
XX
SQ   Sequence   119 AA;


  Query Match             63.3%;  Score 62;  DB 18;  Length 119;
  Best Local Similarity   68.8%;  Pred. No. 0.053;
  Matches   11;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2 RQKYNKRAMDYWGQGT 17
           |  |   |||||||||
Db      98 rhhygyyamdywgqgt 113


RESULT   8
AAR74960
ID   AAR74960 standard; Protein; 133 AA.
XX
AC   AAR74960;
XX
DT   02-FEB-1996  (first entry)
XX
DE   Anti-idiotype antibody Idio3 clone 3GB1.
XX
KW   Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW   complementarity determining region.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..9
FT                   /label= signal_peptide
XX
PN   JP07101999-A.
XX
PD   18-APR-1995.
XX
PF   06-OCT-1993;   93JP-0272950.
XX
PR   06-OCT-1993;   93JP-0272950.
XX
PA   (HAGI/) HAGIWARA Y.
XX
DR   WPI; 1995-182987/24.
DR   N-PSDB; AAQ90425.
XX
PT   Novel anti-idiotype antibody against an human anticancer monoclonal
PT   antibody  - and DNA sequences encoding the antibody, useful in
PT   pharmacology, medicine and biochemical fields.
XX
PS   Example 5; Page 13; 28pp; Japanese.
XX
CC   AAR74960-R74969 are clones of the  anti-idiotype antibodies Idio3,
CC   Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoconal
CC   antibody. These antibodies and DNA encoding them are useful in
CC   pharmacological, medical and biochemical fields of research.
XX
SQ   Sequence   133 AA;
```

```
  Query Match            63.3%;  Score 62;  DB 16;  Length 133;
  Best Local Similarity  52.9%;  Pred. No. 0.059;
  Matches    9;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TRQKYNKRAMDYWGQGT 17
          |:::|:   :|||||||
Db    106 tkeeydydtldywgqgt 122


RESULT   9
AAR74961
ID   AAR74961 standard; Protein; 135 AA.
XX
AC   AAR74961;
XX
DT   02-FEB-1996  (first entry)
XX
DE   Anti-idiotype antibody Idio17 clone 17GB7.
XX
KW   Antibody; cancer; anti-idiotype; CDR; heavy chain; light chain;
KW   immunoglobulin; complementarity determining region.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..10
FT                   /label= signal_peptide
XX
PN   JP07101999-A.
XX
PD   18-APR-1995.
XX
PF   06-OCT-1993;   93JP-0272950.
XX
PR   06-OCT-1993;   93JP-0272950.
XX
PA   (HAGI/) HAGIWARA Y.
XX
DR   WPI; 1995-182987/24.
DR   N-PSDB; AAQ90426.
XX
PT   Novel anti-idiotype antibody against an human anticancer monoclonal
PT   antibody  - and DNA sequences encoding the antibody, useful in
PT   pharmacology, medicine and biochemical fields.
XX
PS   Example 5; Page 14; 28pp; Japanese.
XX
CC   AAR74960-R74969 are clones of the  anti-idiotype antibodies Idio3,
CC   Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoconal
CC   antibody. These antibodies and DNA encoding them are useful in
CC   pharmacological, medical and biochemical fields of research.
XX
SQ   Sequence   135 AA;


  Query Match            63.3%;  Score 62;  DB 16;  Length 135;
  Best Local Similarity  52.9%;  Pred. No. 0.06;
  Matches    9;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TRQKYNKRAMDYWGQGT 17
          |:::|:   :|||||||
Db    107 tkeeydydtldywgqgt 123


RESULT  10
AAY43867
ID   AAY43867 standard; Peptide; 143 AA.
XX
AC   AAY43867;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Heavy chain (VH) gene sequence of Bacillus anthracis antibody 24-2.
XX
KW   Heavy chain; VH; IgG; monoclonal antibody; spore; Bacillus;
KW   VH gene usage; anthrax.
XX
OS   Mus sp.
XX
PN   WO9955842-A1.
XX
PD   04-NOV-1999.
XX
PF   27-APR-1999;   99WO-US09122.
XX
PR   29-APR-1998;   98US-0069628.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Kearney JF;
XX
DR   WPI; 2000-013435/01.
XX
PT   Monoclonal antibody specific for Bacillus spores, used to detect
PT   anthrax  -
XX
PS   Example 13; Page 54; 64pp; English.
XX
CC   AAY43862-75 represent the amino acid sequences of the heavy chain
CC   (VH) gene sequences from antibodies against Bacillus anthracis
CC   spores. The antibodies are produced by different hybridomas. The
CC   specification describes monoclonal antibodies (especially IgG
CC   antibodies) which are highly specific and can discriminate between the
CC   spores of the Bacillus family. The antibodies are produced by exposing
CC   mice to Bacillus spores. The humoral immune response to Bacillus spores
CC   shows a conservation of VH gene usage which is distinct for each spore.
CC   Peptide fragments derived from the antibodies are also capable of
CC   binding spores. The monoclonal antibody, and peptide fragments of it, can
CC   be used to detect Bacillus spores in a field sample. It is particularly
CC   uses for detecting anthrax in a field sample.
XX
SQ   Sequence   143 AA;


  Query Match            63.3%;  Score 62;  DB 21;  Length 143;
  Best Local Similarity  68.8%;  Pred. No. 0.063;
  Matches   11;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 RQKYNKRAMDYWGQGT 17
          ||   : |||||||||
Db     90 rqglrryamdywgqgt 105


RESULT  11
AAY43857
ID   AAY43857 standard; Peptide; 144 AA.
XX
AC   AAY43857;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Heavy chain framework 3 region of antibodies from hybridoma a05.
XX
KW   Heavy chain; VH; IgG; monoclonal antibody; spore; Bacillus;
KW   VH gene usage; anthrax; framework 3.
XX
OS   Mus sp.
XX
PN   WO9955842-A1.
XX
PD   04-NOV-1999.
XX
PF   27-APR-1999;   99WO-US09122.
XX
```

PR 29-APR-1998; 98US-0069628.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Kearney JF;
XX
DR WPI; 2000-013435/01.
XX
PT Monoclonal antibody specific for Bacillus spores, used to detect
PT anthrax -
XX
PS Example 10; Page 46-47; 64pp; English.
XX
CC AAY43851-61 represent the amino acid sequences of the framework 3 (FR3)
CC region of heavy chains from antibodies against Bacillus subtilis
CC spores. The antibodies are produced by different hybridomas. The
CC specification describes monoclonal antibodies (especially IgG
CC antibodies) which are highly specific and can discriminate between the
CC spores of the Bacillus family. The antibodies are produced by exposing
CC mice to Bacillus spores. The humoral immune response to Bacillus spores
CC shows a conservation of VH gene usage which is distinct for each spore.
CC Peptide fragments derived from the antibodies are also capable of
CC binding spores. The monoclonal antibody, and peptide fragments of it, can
CC be used to detect Bacillus spores in a field sample. It is particularly
CC uses for detecting anthrax in a field sample.
XX
SQ Sequence 144 AA;

Query Match 63.3%; Score 62; DB 21; Length 144;
Best Local Similarity 83.3%; Pred. No. 0.063;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NKRAMDYWGQGT 17
:|||:|||||||
Db 95 skraidywgqgt 106

RESULT 12
AAY91026
ID AAY91026 standard; Protein; 436 AA.
XX
AC AAY91026;
XX
DT 05-SEP-2000 (first entry)
XX
DE Apoptobody3sc fusion protein SEQ ID NO:8.
XX
KW Human; Fas antigen; apoptosis; apoptobody3sc; antibody; fusion gene;
KW medical; pharmaceutical; pharmacological; biochemical.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN JP2000102389-A.
XX
PD 11-APR-2000.
XX
PF 29-SEP-1998; 98JP-0291441.
XX
PR 29-SEP-1998; 98JP-0291441.
XX
PA (HAGI/) HAGIWARA Y.
PA (HAGI/) HAGIWARA H.
XX
DR WPI; 2000-332086/29.
DR N-PSDB; AAA39167.
XX
PT Causing apoptosis comprises transfecting fused gene to cell and
PT reacting cell with idiotypic antibody -
XX
PS Disclosure; Page 8-9; 10pp; Japanese.
XX
CC The present invention describes a method for causing apoptosis in which
CC a fused gene consisting of a gene participating to apoptosis and a gene
CC encoding at least the variable region of anti-idiotype antibody is
CC transfected to a cell to express the fused gene and then an idiotype
CC antibody is reacted with the expressed cell. The method is useful in
CC medical, pharmaceutical, pharmacological and biochemical fields. The
CC present sequence represents a fusion protein designated apoptobody3sc,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 436 AA;

Query Match 63.3%; Score 62; DB 21; Length 436;
Best Local Similarity 52.9%; Pred. No. 0.19;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TRQKYNKRAMDYWGQGT 17
|:::|: :|||||||
Db 250 tkeeydydtldywgqgt 266

RESULT 13
AAR25730
ID AAR25730 standard; Protein; 119 AA.
XX
AC AAR25730;
XX
DT 13-JAN-1993 (first entry)
XX
DE Humanised VH region of the mouse CMV5 antibody.
XX
KW Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
KW gH; heavy chain; variable region; framework; human; Wol.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT /note= "CDR"
FT Region 50..66
FT /note= "CDR"
FT Region 99..108
FT /note= "CDR"
FT Misc-difference 5
FT /note= "mutated residue"
FT Misc-difference 24
FT /note= "mutated residue"
FT Misc-difference 27
FT /note= "mutated residue"
FT Misc-difference 28
FT /note= "mutated residue"
FT Misc-difference 30
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FT Misc-difference 80
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FT Misc-difference 97
FT /note= "mutated residue"
XX
PN WO9211018-A.
XX
PD 09-JUL-1992.
XX
PF 19-DEC-1991; 91WO-US09711.
XX
PR 19-DEC-1990; 90US-0634278.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Co MS, Coelingh KL, Landolfi NF, Queen CL, Schneider WP;
XX
DR WPI; 1992-249842/30.

```
XX
PT   New immunoglobulin(s) having murine CDRs in human framework
PT   regions - have lower antigenicity; useful for treating e.g. HSV,
PT   CMV, T-cell disorders, myeloid disorders and auto-immune
PT   conditions
XX
PS   Claim 40; Fig 27B; 141pp; English.
XX
CC   The sequence shows the humanised mature heavy chain variable
CC   region of the mouse CMV5 antibody.  Murine CDRs were used
CC   in a human Wol framework to produce a pure humanised immunoglobulin
CC   (Ig) which is capable of binding to the gH glycoprotein of
CC   cytomegalovirus.  The Ig is non immunogenic, due to the human
CC   framework, and has a strong affinity for its predetermined
CC   antigen.  They can be produced in large quantities via recombinant
CC   DNA and monoclonal antibody technology. The humanised Igs may be
CC   used alone or in combination with chemotherapeutic agents such as
CC   non-steroidal anti-inflammatory drugs or immunosuppressants.
CC   See also AAR25721-32.
XX
SQ   Sequence   119 AA;

  Query Match             62.2%;  Score 61;  DB 13;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.074;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :||||||||
Db      97 trrgfrdysmdywgqgt 113


RESULT  14
AAB69679
ID   AAB69679 standard; Protein; 119 AA.
XX
AC   AAB69679;
XX
DT   30-APR-2001  (first entry)
XX
DE   Murine CMV5 antibody heavy chain SEQ ID NO: 64.
XX
KW   Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KW   light chain; graft versus host disease; transplant; autoimmune disease;
KW   multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW   myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX
OS   Mus sp.
XX
PN   US6180370-B1.
XX
PD   30-JAN-2001.
XX
PF   07-JUN-1995;   95US-0484537.
XX
PR   28-DEC-1988;   88US-0290975.
PR   13-FEB-1989;   89US-0310252.
PR   28-SEP-1990;   90US-0590274.
PR   19-DEC-1990;   90US-0634278.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Queen CL,  Selick HE;
XX
DR   WPI; 2001-190856/19.
XX
PT   Producing humanized immunoglobulin, involves producing a cell
PT   containing DNA segments encoding humanized heavy and light chain
PT   variable regions, and expressing the DNA segments in the cell -
XX
PS   Disclosure; Fig 6; 145pp; English.
XX
CC   The present invention describes a method of producing humanised
CC   immunoglobulins involving expressing in a cell a nucleic acid encoding a
CC   humanised version of an immunoglobulin. This is obtained by comparing a
CC   donor and human immunoglobulin and producing a combined antibody which
CC   contains part of each. These are useful in the treatment of
CC   graft-versus-host disease, transplant rejection, autoimmune diseases such
CC   as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
CC   and systemic lupus erythematosus, herpes infections, CMV virus infections
CC   and myeloid leukaemia. THe present sequence is an antibody used to
CC   demonstrate the method of the invention.
XX
SQ   Sequence   119 AA;


  Query Match             62.2%;  Score 61;  DB 22;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.074;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :||||||||
Db      97 trrgfrdysmdywgqgt 113


RESULT  15
AAB69680
ID   AAB69680 standard; Protein; 119 AA.
XX
AC   AAB69680;
XX
DT   30-APR-2001  (first entry)
XX
DE   Humanised CMV5 antibody heavy chain SEQ ID NO: 65.
XX
KW   Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KW   light chain; graft versus host disease; transplant; autoimmune disease;
KW   multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW   myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   US6180370-B1.
XX
PD   30-JAN-2001.
XX
PF   07-JUN-1995;   95US-0484537.
XX
PR   28-DEC-1988;   88US-0290975.
PR   13-FEB-1989;   89US-0310252.
PR   28-SEP-1990;   90US-0590274.
PR   19-DEC-1990;   90US-0634278.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Queen CL,  Selick HE;
XX
DR   WPI; 2001-190856/19.
XX
PT   Producing humanized immunoglobulin, involves producing a cell
PT   containing DNA segments encoding humanized heavy and light chain
PT   variable regions, and expressing the DNA segments in the cell -
XX
PS   Disclosure; Fig 6; 145pp; English.
XX
CC   The present invention describes a method of producing humanised
CC   immunoglobulins involving expressing in a cell a nucleic acid encoding a
CC   humanised version of an immunoglobulin. This is obtained by comparing a
CC   donor and human immunoglobulin and producing a combined antibody which
CC   contains part of each. These are useful in the treatment of
CC   graft-versus-host disease, transplant rejection, autoimmune diseases such
CC   as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
CC   and systemic lupus erythematosus, herpes infections, CMV virus infections
CC   and myeloid leukaemia. THe present sequence is an antibody used to
CC   demonstrate the method of the invention.
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XX
SQ Sequence 119 AA;

Query Match 62.2%; Score 61; DB 22; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.074;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :||||||||
Db      97 trrgfrdysmdywgqgt 113
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Search completed: June 27, 2001, 11:29:17
Job time: 57 sec

GenCore version 4.5


OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:20 ; Search time 11.81 Seconds
(without alignments)
28.997 Million cell updates/sec

Title: US-09-497-997B-1
Perfect score: 98
Sequence: 1 TRQKYNKRAMDYWGQGT 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
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| 1 | 64 | 65.3 | 140 | 3 | US-08-836-561-23 | Sequence 23, Appl |
| 2 | 62 | 63.3 | 119 | 4 | US-08-767-128-6 | Sequence 6, Appli |
| 3 | 61 | 62.2 | 115 | 2 | US-08-379-057-31 | Sequence 31, Appl |
| 4 | 61 | 62.2 | 118 | 2 | US-08-379-057-30 | Sequence 30, Appl |
| 5 | 61 | 62.2 | 119 | 1 | US-07-634-278-64 | Sequence 64, Appl |
| 6 | 61 | 62.2 | 119 | 1 | US-07-634-278-65 | Sequence 65, Appl |
| 7 | 61 | 62.2 | 119 | 1 | US-07-634-278-89 | Sequence 89, Appl |
| 8 | 61 | 62.2 | 119 | 1 | US-08-477-728-64 | Sequence 64, Appl |
| 9 | 61 | 62.2 | 119 | 1 | US-08-477-728-65 | Sequence 65, Appl |
| 10 | 61 | 62.2 | 119 | 1 | US-08-477-728-89 | Sequence 89, Appl |
| 11 | 61 | 62.2 | 119 | 1 | US-08-474-040-64 | Sequence 64, Appl |
| 12 | 61 | 62.2 | 119 | 1 | US-08-474-040-65 | Sequence 65, Appl |
| 13 | 61 | 62.2 | 119 | 1 | US-08-474-040-89 | Sequence 89, Appl |
| 14 | 61 | 62.2 | 119 | 1 | US-08-487-200-64 | Sequence 64, Appl |
| 15 | 61 | 62.2 | 119 | 1 | US-08-487-200-65 | Sequence 65, Appl |
| 16 | 61 | 62.2 | 119 | 1 | US-08-487-200-89 | Sequence 89, Appl |
| 17 | 61 | 62.2 | 119 | 4 | US-08-484-537-64 | Sequence 64, Appl |
| 18 | 61 | 62.2 | 119 | 4 | US-08-484-537-65 | Sequence 65, Appl |
| 19 | 61 | 62.2 | 119 | 4 | US-08-484-537-89 | Sequence 89, Appl |
| 20 | 61 | 62.2 | 138 | 1 | US-07-634-278-85 | Sequence 85, Appl |
| 21 | 61 | 62.2 | 138 | 1 | US-08-477-728-85 | Sequence 85, Appl |
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| 26 | 60 | 61.2 | 118 | 2 | US-08-553-497A-16 | Sequence 16, Appl |
| 27 | 59 | 60.2 | 118 | 2 | US-08-888-366-4 | Sequence 4, Appli |
| 28 | 59 | 60.2 | 118 | 5 | PCT-US93-08435-10 | Sequence 10, Appl |
| 29 | 59 | 60.2 | 122 | 5 | PCT-US93-08435-12 | Sequence 12, Appl |
| 30 | 59 | 60.2 | 122 | 5 | PCT-US93-08435-14 | Sequence 14, Appl |
| 31 | 59 | 60.2 | 122 | 5 | PCT-US93-08435-43 | Sequence 43, Appl |
| 32 | 59 | 60.2 | 124 | 4 | US-08-767-128-38 | Sequence 38, Appl |
| 33 | 58 | 59.2 | 115 | 3 | US-08-881-037-22 | Sequence 22, Appl |
| 34 | 58 | 59.2 | 121 | 3 | US-08-881-037-67 | Sequence 67, Appl |
| 35 | 58 | 59.2 | 123 | 2 | US-08-561-521-9 | Sequence 9, Appli |
| 36 | 58 | 59.2 | 123 | 2 | US-08-561-521-11 | Sequence 11, Appl |
| 37 | 58 | 59.2 | 123 | 5 | PCT-US95-01219-9 | Sequence 9, Appli |
| 38 | 58 | 59.2 | 123 | 5 | PCT-US95-01219-11 | Sequence 11, Appl |
| 39 | 58 | 59.2 | 140 | 2 | US-08-561-521-4 | Sequence 4, Appli |
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| 41 | 58 | 59.2 | 142 | 2 | US-08-561-521-17 | Sequence 17, Appl |
| 42 | 58 | 59.2 | 142 | 5 | PCT-US95-01219-17 | Sequence 17, Appl |
| 43 | 56.5 | 57.7 | 222 | 2 | US-08-737-129A-6 | Sequence 6, Appli |
| 44 | 56 | 57.1 | 116 | 1 | US-08-401-908-1 | Sequence 1, Appli |
| 45 | 56 | 57.1 | 116 | 4 | US-08-397-411-3 | Sequence 3, Appli |

ALIGNMENTS

```
RESULT   1
US-08-836-561-23
; Sequence 23, Application US/08836561
; Patent No. 6018032
;  GENERAL INFORMATION:
;    APPLICANT:  KOIKE, Masamichi
;    APPLICANT:  FURUYA, Akiko
;    APPLICANT:  NAKAMURA, Kazuyasu
;    APPLICANT:  IIDA, Akihiro
;    APPLICANT:  ANAZAWA, Hideharu
;    APPLICANT:  HANAI, No. 6018032uo
;    APPLICANT:  TAKATSU, Kiyoshi
;    TITLE OF INVENTION:  Antibody Against Human Interleukin-5
;    TITLE OF INVENTION:  Receptor Alpha Chain
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,561
;      FILING DATE:  09-MAY-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 232384/95
;      FILING DATE:  11-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lawrence, III, Stanton T
;      REGISTRATION NUMBER:  25,736
;      REFERENCE/DOCKET NUMBER:  7005-115-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  140 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
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US-08-836-561-23

Query Match 65.3%; Score 64; DB 3; Length 140;
Best Local Similarity 91.7%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       6 NKRAMDYWGQGT 17
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Db     123 NYRAMDYWGQGT 134
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RESULT 2
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 63.3%; Score 62; DB 4; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       2 RQKYNKRAMDYWGQGT 17
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Db      98 RHHYGYYAMDYWGQGT 113
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RESULT 3
US-08-379-057-31
; Sequence 31, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,057
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0133-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-379-057-31

Query Match 62.2%; Score 61; DB 2; Length 115;
Best Local Similarity 76.9%; Pred. No. 0.023;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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           |: |||||||||
Db      98 YDSYAMDYWGQGT 110
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RESULT 4
US-08-379-057-30
; Sequence 30, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:

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;    APPLICANT:  Siadak, Anthony W.
;    APPLICANT:  Hollenbaugh, Diane L.
;    APPLICANT:  Gilliland, Lisa K.
;    APPLICANT:  Gordon, Marcia L.
;    APPLICANT:  Bajorath, Jurgen
;    APPLICANT:  Aruffo, Alejandro A.
;    TITLE OF INVENTION:  Monoclonal Antibodies Specific For
;    TITLE OF INVENTION:  Different Epitopes of Human gp39 and Methods For Their Use
;    TITLE OF INVENTION:  In Diagnosis and Therapy
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/379,057
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poor, Brian W.
;      REGISTRATION NUMBER:  32,928
;      REFERENCE/DOCKET NUMBER:  ON0133-
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 727-3670
;      TELEFAX:  (206) 727-3601
;  INFORMATION FOR SEQ ID NO:  30:
;  . SEQUENCE CHARACTERISTICS:
;      LENGTH:  118 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-379-057-30


  Query Match             62.2%;  Score 61;  DB 2;  Length 118;
  Best Local Similarity   76.9%;  Pred. No. 0.024;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 YNKRAMDYWGQGT 17
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Db     101 YDSYAMDYWGQGT 113


RESULT   5
US-07-634-278-64
; Sequence 64, Application US/07634278
; Patent No. 5530101
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-634-278-64


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
             ||: :   :|||||||||
Db      97 TRRGFRDYSMDYWGQGT 113


RESULT   6
US-07-634-278-65
; Sequence 65, Application US/07634278
; Patent No. 5530101
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-634-278-65


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :||||||||
Db      97 TRRGFRDYSMDYWGQGT 113


RESULT   7
US-07-634-278-89
; Sequence 89, Application US/07634278
; Patent No. 5530101
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-634-278-89


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :||||||||
Db      97 TRRGFRDYSMDYWGQGT 113


RESULT   8
US-08-477-728-64
; Sequence 64, Application US/08477728
; Patent No. 5585089
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,728
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
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;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-477-728-64


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 TRQKYNKRAMDYWGQGT 17
          ||: :   :|||||||
Db     97 TRRGFRDYSMDYWGQGT 113


RESULT   9
US-08-477-728-65
; Sequence 65, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,728
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-477-728-65


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 TRQKYNKRAMDYWGQGT 17
          ||: :   :|||||||
Db     97 TRRGFRDYSMDYWGQGT 113


RESULT  10
US-08-477-728-89
; Sequence 89, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,728
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-477-728-89


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 TRQKYNKRAMDYWGQGT 17
          ||: :   :|||||||
Db     97 TRRGFRDYSMDYWGQGT 113


RESULT  11
US-08-474-040-64
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; Sequence 64, Application US/08474040
; Patent No. 5693761
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,040
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-474-040-64


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :||||||||
Db      97 TRRGFRDYSMDYWGQGT 113


RESULT  12
US-08-474-040-65
; Sequence 65, Application US/08474040
; Patent No. 5693761
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,040
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-474-040-65


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :||||||||
Db      97 TRRGFRDYSMDYWGQGT 113


RESULT  13
US-08-474-040-89
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; Patent No. 5693761
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
```

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;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,040
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-474-040-89


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :|||||||||
Db      97 TRRGFRDYSMDYWGQGT 113


RESULT  14
US-08-487-200-64
; Sequence 64, Application US/08487200
; Patent No. 5693762
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,200
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002610
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-487-200-64


  Query Match             62.2%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   58.8%;  Pred. No. 0.024;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :|||||||||
Db      97 TRRGFRDYSMDYWGQGT 113


RESULT  15
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; Patent No. 5693762
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,200
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  424
```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; ORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-65

Query Match 62.2%; Score 61; DB 1; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.024;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy       1 TRQKYNKRAMDYWGQGT 17
           ||: :   :||||||||
Db      97 TRRGFRDYSMDYWGQGT 113
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Search completed: June 27, 2001, 11:28:37
Job time: 17 sec

GenCore version 4.5


OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:40 ; Search time 21.08 Seconds
(without alignments)
106.698 Million cell updates/sec

Title: US-09-497-997B-1
Perfect score: 98
Sequence: 1 TRQKYNKRAMDYWGQGT 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 58.5 | 59.7 | 110 | 11 | Q9JL77 | Q9jl77 mus musculu |
| 2 | 56 | 57.1 | 117 | 11 | Q9QXE9 | Q9qxe9 mus musculu |
| 3 | 55.5 | 56.6 | 112 | 4 | Q9HCC1 | Q9hcc1 homo sapien |
| 4 | 55 | 56.1 | 109 | 11 | Q9JL75 | Q9jl75 mus musculu |
| 5 | 53 | 54.1 | 118 | 4 | Q9UL72 | Q9ul72 homo sapien |
| 6 | 50 | 51.0 | 321 | 2 | Q9KR64 | Q9kr64 vibrio chol |
| 7 | 49 | 50.0 | 147 | 4 | Q9Y509 | Q9y509 homo sapien |
| 8 | 48 | 49.0 | 119 | 5 | Q9GYZ2 | Q9gyz2 schistosoma |
| 9 | 46 | 46.9 | 109 | 11 | Q9JL85 | Q9jl85 mus musculu |
| 10 | 46 | 46.9 | 113 | 4 | Q9UL90 | Q9ul90 homo sapien |
| 11 | 46 | 46.9 | 114 | 11 | Q9JL81 | Q9jl81 mus musculu |
| 12 | 46 | 46.9 | 117 | 11 | Q9QXF0 | Q9qxf0 mus musculu |
| 13 | 46 | 46.9 | 118 | 11 | Q9Z1C4 | Q9z1c4 mus musculu |
| 14 | 46 | 46.9 | 119 | 4 | Q9UL73 | Q9ul73 homo sapien |
| 15 | 46 | 46.9 | 121 | 4 | Q9UL96 | Q9ul96 homo sapien |
| 16 | 46 | 46.9 | 122 | 4 | Q9UL84 | Q9ul84 homo sapien |
| 17 | 46 | 46.9 | 122 | 4 | Q9UL75 | Q9ul75 homo sapien |
| 18 | 46 | 46.9 | 124 | 4 | Q9UL92 | Q9ul92 homo sapien |
| 19 | 46 | 46.9 | 314 | 2 | P74237 | P74237 synechocyst |
| 20 | 46 | 46.9 | 384 | 4 | Q9UP60 | Q9up60 homo sapien |
| 21 | 45 | 45.9 | 1031 | 2 | Q9WXJ2 | Q9wxj2 psychromona |
| 22 | 44 | 44.9 | 131 | 4 | Q9UL88 | Q9ul88 homo sapien |
| 23 | 44 | 44.9 | 377 | 7 | Q9GIW6 | Q9giw6 ictalurus p |
| 24 | 44 | 44.9 | 401 | 5 | O01602 | O01602 caenorhabdi |
| 25 | 44 | 44.9 | 436 | 10 | O22949 | O22949 arabidopsis |
| 26 | 44 | 44.9 | 658 | 11 | Q9QWS9 | Q9qws9 mus musculu |
| 27 | 44 | 44.9 | 739 | 2 | Q9X687 | Q9x687 salmonella |
| 28 | 43 | 43.9 | 27 | 14 | Q78983 | Q78983 human immun |
| 29 | 43 | 43.9 | 27 | 14 | Q78989 | Q78989 human immun |
| 30 | 43 | 43.9 | 118 | 4 | Q9UL91 | Q9ul91 homo sapien |
| 31 | 43 | 43.9 | 196 | 14 | Q9WGP1 | Q9wgp1 human immun |
| 32 | 43 | 43.9 | 218 | 14 | Q9YIU8 | Q9yiu8 human immun |
| 33 | 43 | 43.9 | 218 | 14 | Q9WBH8 | Q9wbh8 human immun |
| 34 | 43 | 43.9 | 328 | 14 | Q9EL95 | Q9el95 human immun |
| 35 | 43 | 43.9 | 328 | 14 | Q9EID8 | Q9eid8 human immun |
| 36 | 43 | 43.9 | 328 | 14 | Q9EHY2 | Q9ehy2 human immun |
| 37 | 43 | 43.9 | 328 | 14 | Q9EGX2 | Q9egx2 human immun |
| 38 | 43 | 43.9 | 328 | 14 | Q9EFW2 | Q9efw2 human immun |
| 39 | 43 | 43.9 | 328 | 14 | Q9EE99 | Q9ee99 human immun |
| 40 | 43 | 43.9 | 328 | 14 | Q9ECP1 | Q9ecp1 human immun |
| 41 | 43 | 43.9 | 328 | 14 | Q9ECC1 | Q9ecc1 human immun |
| 42 | 43 | 43.9 | 416 | 4 | Q9NPP6 | Q9npp6 homo sapien |
| 43 | 43 | 43.9 | 566 | 2 | P94189 | P94189 alcaligenes |
| 44 | 43 | 43.9 | 1095 | 5 | O01478 | O01478 caenorhabdi |
| 45 | 42 | 42.9 | 118 | 4 | Q9UL74 | Q9ul74 homo sapien |

ALIGNMENTS

RESULT 1
Q9JL77
ID Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF206029; AAF69327.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 59.7%; Score 58.5; DB 11; Length 110;
Best Local Similarity 75.0%; Pred. No. 0.027;
Matches 12; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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Qy       2 RQKYNKRAMDYWGQGT 17
           ||: |  |||||||||
Db      90 RQRRN-YAMDYWGQGT 104
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RESULT 2
Q9QXE9
ID Q9QXE9 PRELIMINARY; PRT; 117 AA.
AC Q9QXE9;

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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ225174; CAB65237.1; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13000 MW;  CDDE2AF84D499734 CRC64;

  Query Match             57.1%;  Score 56;  DB 11;  Length 117;
  Best Local Similarity   68.8%;  Pred. No. 0.073;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    2;  Gaps    1;

Qy       2 RQKYNKRAMDYWGQGT 17
           | :|   |||||||||
Db      98 RDRY--YAMDYWGQGT 111


RESULT   3
Q9HCC1
ID   Q9HCC1      PRELIMINARY;      PRT;   112 AA.
AC   Q9HCC1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT   "An antibody fragment2A3 specific for native lysozyme :Isolaion from a
RT   human synthetic phage display library and characterization.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB049915; BAB16829.1; -.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  12243 MW;  24F1A45EC3B84788 CRC64;

  Query Match             56.6%;  Score 55.5;  DB 4;  Length 112;
  Best Local Similarity   62.5%;  Pred. No. 0.085;
  Matches   10;  Conservative    3;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       2 RQKYNKRAMDYWGQGT 17
           |::|   |:|||||||
Db      98 RRRY---ALDYWGQGT 110


RESULT   4
Q9JL75
ID   Q9JL75      PRELIMINARY;      PRT;   109 AA.
AC   Q9JL75;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF206031; AAF69329.1; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  12118 MW;  FF65E441BBF936A6 CRC64;

  Query Match             56.1%;  Score 55;  DB 11;  Length 109;
  Best Local Similarity   75.0%;  Pred. No. 0.099;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       6 NKRAMDYWGQGT 17
           | |  |||||||
Db      92 NYRGFDYWGQGT 103


RESULT   5
Q9UL72
ID   Q9UL72      PRELIMINARY;      PRT;   118 AA.
AC   Q9UL72;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035042; AAD56278.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  12872 MW;  B4D1A5944B2D5CCA CRC64;

  Query Match             54.1%;  Score 53;  DB 4;  Length 118;
  Best Local Similarity   50.0%;  Pred. No. 0.23;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2 RQKYNKRAMDYWGQGT 17
           | :: :   |||||||
Db      97 RDRFGEFLFDYWGQGT 112


RESULT   6
Q9KR64
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ID   Q9KR64      PRELIMINARY;      PRT;   321 AA.
AC   Q9KR64;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   C4-DICARBOXYLATE-BINDING PERIPLASMIC PROTEIN.
GN   VC1779.
OS   Vibrio cholerae.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX   NCBI_TaxID=666;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EL TOR N16961 / SEROTYPE O1;
RX   MEDLINE=20406833; PubMed=10952301;
RA   Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA   Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA   Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA   Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA   McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
RA   Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA   Fraser C.M.;
RT   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT   cholerae.";
RL   Nature 406:477-483(2000).
DR   EMBL; AE004255; AAF94928.1; -.
DR   TIGR; VC1779; -.
SQ   SEQUENCE   321 AA;  35982 MW;  C1A44BB820F595F0 CRC64;


  Query Match             51.0%;  Score 50;  DB 2;  Length 321;
  Best Local Similarity   60.0%;  Pred. No. 2.2;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 QKYNKRAMDYWGQGT 17
           ||:| ||:| |  ||
Db     132 QKFNWRALDTWYNGT 146


RESULT   7
Q9Y509
ID   Q9Y509      PRELIMINARY;      PRT;   147 AA.
AC   Q9Y509;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VH3 PROTEIN (FRAGMENT).
GN   VH3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96071149; PubMed=7475288;
RA   Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA   Lichtenstein A.K., Berenson J.R.;
RT   "A CD10-positive subset of malignant cells is identified in multiple
RT   myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL   Leukemia 9:1948-1953(1995).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; S80860; AAD14339.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   147 AA;  15768 MW;  8489FCAAA7BC925C CRC64;


  Query Match             50.0%;  Score 49;  DB 4;  Length 147;
  Best Local Similarity   61.5%;  Pred. No. 1.3;
  Matches    8;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       5 YNKRAMDYWGQGT 17
           |    :|||||||
Db     108 YYYAGIDYWGQGT 120


RESULT   8
Q9GYZ2
ID   Q9GYZ2      PRELIMINARY;      PRT;   119 AA.
AC   Q9GYZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC   Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC   Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the heavy chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF282622; AAG01452.1; -.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13567 MW;  BA893873FD5FA6AB CRC64;


  Query Match             49.0%;  Score 48;  DB 5;  Length 119;
  Best Local Similarity   87.5%;  Pred. No. 1.5;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      10 MDYWGQGT 17
           :|||||||
Db     106 LDYWGQGT 113


RESULT   9
Q9JL85
ID   Q9JL85      PRELIMINARY;      PRT;   109 AA.
AC   Q9JL85;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF206021; AAF69319.1; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11944 MW;  DFE615FE6CED4EDE CRC64;


  Query Match             46.9%;  Score 46;  DB 11;  Length 109;
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  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 DYWGQGT 17
           |||||||
Db      97 DYWGQGT 103


RESULT  10
Q9UL90
ID   Q9UL90      PRELIMINARY;      PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035024; AAD56260.1; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;


  Query Match             46.9%;  Score 46;  DB 4;  Length 113;
  Best Local Similarity   53.8%;  Pred. No. 3.1;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 YNKRAMDYWGQGT 17
           |  : ::|||||||
Db      95 YCAKDLNYWGQGT 107


RESULT  11
Q9JL81
ID   Q9JL81      PRELIMINARY;      PRT;   114 AA.
AC   Q9JL81;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF206025; AAF69323.1; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     114    114
SQ   SEQUENCE   114 AA;  12829 MW;  404885FDE6BA56F8 CRC64;


  Query Match             46.9%;  Score 46;  DB 11;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 DYWGQGT 17
           |||||||
Db     102 DYWGQGT 108


RESULT  12
Q9QXF0
ID   Q9QXF0      PRELIMINARY;      PRT;   117 AA.
AC   Q9QXF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ225171; CAB65236.1; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13060 MW;  D816AD0858A47E4C CRC64;


  Query Match             46.9%;  Score 46;  DB 11;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 DYWGQGT 17
           |||||||
Db     105 DYWGQGT 111


RESULT  13
Q9Z1C4
ID   Q9Z1C4      PRELIMINARY;      PRT;   118 AA.
AC   Q9Z1C4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA   Matis L.M., Evans M.J.;
RT   "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT   IgG2/G4 constant regions block human leukocyte binding to porcine
RT   endothelial cells.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; U78801; AAD00293.1; -.
```

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DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13036 MW;  90EEC559D31EC4FC CRC64;


  Query Match             46.9%;  Score 46;  DB 11;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     11 DYWGQGT 17
          |||||||
Db    106 DYWGQGT 112


RESULT  14
Q9UL73
ID   Q9UL73      PRELIMINARY;      PRT;   119 AA.
AC   Q9UL73;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035041; AAD56277.1; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13219 MW;  1BDB86B6420EA0BE CRC64;


  Query Match             46.9%;  Score 46;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     11 DYWGQGT 17
          |||||||
Db    107 DYWGQGT 113


RESULT  15
Q9UL96
ID   Q9UL96      PRELIMINARY;      PRT;   121 AA.
AC   Q9UL96;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035018; AAD56254.1; -.
DR   InterPro; IPR003006; -.
DR   InterPro; IPR003596; -.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13695 MW;  D582D450596BDD35 CRC64;


  Query Match             46.9%;  Score 46;  DB 4;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     11 DYWGQGT 17
          |||||||
Db    109 DYWGQGT 115


Search completed: June 27, 2001, 11:33:10
Job time: 270 sec
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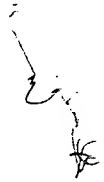

GenCore version 4.5


OM protein - protein search, using sw model

Run on: June 27, 2001, 11:28:55 ; Search time 8.3 Seconds
(without alignments)
70.162 Million cell updates/sec

Title: US-09-497-997B-1
Perfect score: 98
Sequence: 1 TRQKYNKRAMDYWGQGT 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 56 | 57.1 | 136 | 1 | HV16_MOUSE | P01783 mus musculu |
| 2 | 51 | 52.0 | 122 | 1 | HV3G_HUMAN | P01768 homo sapien |
| 3 | 50 | 51.0 | 117 | 1 | HV42_MOUSE | P01812 mus musculu |
| 4 | 50 | 51.0 | 139 | 1 | HV07_MOUSE | P01751 mus musculu |
| 5 | 49 | 50.0 | 136 | 1 | HV15_MOUSE | P01759 mus musculu |
| 6 | 49 | 50.0 | 137 | 1 | HV11_MOUSE | P01755 mus musculu |
| 7 | 48 | 49.0 | 144 | 1 | HV43_MOUSE | P01819 mus musculu |
| 8 | 47.5 | 48.5 | 135 | 1 | HV02_XENLA | P20957 xenopus lae |
| 9 | 46 | 46.9 | 111 | 1 | HV35_MOUSE | P01804 mus musculu |
| 10 | 46 | 46.9 | 116 | 1 | HV3T_HUMAN | P01781 homo sapien |
| 11 | 46 | 46.9 | 118 | 1 | HV39_MOUSE | P01809 mus musculu |
| 12 | 46 | 46.9 | 120 | 1 | HV03_MOUSE | P01747 mus musculu |
| 13 | 46 | 46.9 | 120 | 1 | HV1H_HUMAN | P80421 homo sapien |
| 14 | 46 | 46.9 | 126 | 1 | HV3K_HUMAN | P01772 homo sapien |
| 15 | 46 | 46.9 | 137 | 1 | HV46_MOUSE | P01822 mus musculu |
| 16 | 46 | 46.9 | 140 | 1 | HV02_MOUSE | P01746 mus musculu |
| 17 | 44.5 | 45.4 | 984 | 1 | L100_ADEG1 | Q64760 avian adeno |
| 18 | 44 | 44.9 | 115 | 1 | HV3S_HUMAN | P01780 homo sapien |
| 19 | 44 | 44.9 | 122 | 1 | HV3H_HUMAN | P01769 homo sapien |
| 20 | 44 | 44.9 | 124 | 1 | HV1E_HUMAN | P01761 homo sapien |
| 21 | 43.5 | 44.4 | 113 | 1 | HV27_MOUSE | P01796 mus musculu |
| 22 | 43.5 | 44.4 | 113 | 1 | HV28_MOUSE | P01797 mus musculu |
| 23 | 43.5 | 44.4 | 113 | 1 | HV29_MOUSE | P01798 mus musculu |
| 24 | 43.5 | 44.4 | 113 | 1 | HV30_MOUSE | P01799 mus musculu |
| 25 | 43.5 | 44.4 | 115 | 1 | HV32_MOUSE | P01801 mus musculu |
| 26 | 43 | 43.9 | 117 | 1 | HV2B_RABIT | P01828 oryctolagus |
| 27 | 43 | 43.9 | 142 | 1 | HV01_RAT | P01805 rattus norv |
| 28 | 43 | 43.9 | 146 | 1 | HV2I_HUMAN | P06331 homo sapien |
| 29 | 43 | 43.9 | 201 | 1 | FABG_BRANA | P27582 brassica na |
| 30 | 43 | 43.9 | 779 | 1 | YU20_ARATH | Q9zpv5 arabidopsis |
| 31 | 42.5 | 43.4 | 549 | 1 | YST1_CAEEL | Q22000 caenorhabdi |
| 32 | 42.5 | 43.4 | 897 | 1 | APG1_YEAST | P53104 saccharomyc |
| 33 | 42 | 42.9 | 89 | 1 | HV02_HETFR | P04215 heterodontu |
| 34 | 42 | 42.9 | 114 | 1 | HV01_CANFA | P01784 canis famil |
| 35 | 42 | 42.9 | 115 | 1 | HV3D_HUMAN | P01765 homo sapien |
| 36 | 42 | 42.9 | 116 | 1 | HV3R_HUMAN | P01779 homo sapien |
| 37 | 42 | 42.9 | 118 | 1 | HV3V_HUMAN | P80419 homo sapien |
| 38 | 42 | 42.9 | 121 | 1 | HV2E_HUMAN | P01818 homo sapien |
| 39 | 42 | 42.9 | 121 | 1 | HV3J_HUMAN | P01771 homo sapien |
| 40 | 42 | 42.9 | 147 | 1 | HV2H_HUMAN | P04438 homo sapien |
| 41 | 42 | 42.9 | 501 | 1 | YPWA_BACSU | P50848 bacillus su |
| 42 | 42 | 42.9 | 516 | 1 | YIJ7_YEAST | P40492 saccharomyc |
| 43 | 42 | 42.9 | 655 | 1 | IDUA_CANFA | Q01634 canis famil |
| 44 | 42 | 42.9 | 1147 | 1 | NRDC_HUMAN | O43847 homo sapien |
| 45 | 42 | 42.9 | 1161 | 1 | NRDC_RAT | P47245 rattus norv |

ALIGNMENTS

```
RESULT   1
HV16_MOUSE
ID   HV16_MOUSE     STANDARD;      PRT;   136 AA.
AC   P01783;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
RN   [2]
RP   SEQUENCE OF 17-136.
RX   MEDLINE=77100368; PubMed=401950;
RA   Adetugbo K., Milstein C., Secher D.S.;
RT   "Molecular analysis of spontaneous somatic mutants.";
RL   Nature 265:299-304(1977).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00522; AAD15290.1; -.
DR   PIR; A02066; G1MS21.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     16
FT   CHAIN        17    136       IG HEAVY CHAIN V REGION MOPC 21.
FT   DOMAIN      115    119       D SEGMENT.
FT   DOMAIN      120    136       JH4 SEGMENT.
FT   DISULFID     38    112
FT   CONFLICT     75     78       HYAD -> DYAH (IN REF. 2).
FT   CONFLICT     89     90       DN -> ND (IN REF. 2).
FT   CONFLICT    115    115       W -> H (IN REF. 2).
FT   CONFLICT    120    120       Y -> W (IN REF. 2).
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15071 MW;  2276A98DBDBF7016 CRC64;


  Query Match             57.1%;  Score 56;  DB 1;  Length 136;
  Best Local Similarity   76.9%;  Pred. No. 0.019;
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  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 YNKRAMDYWGQGT 17
           |   |||||||||
Db     118 YPYYAMDYWGQGT 130


RESULT   2
HV3G_HUMAN
ID   HV3G_HUMAN     STANDARD;      PRT;   122 AA.
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V-III REGION CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81013859; PubMed=6774332;
RA   Lehman D.W., Putnam F.W.;
RT   "Amino acid sequence of the variable region of a human mu chain:
RT   location of a possible JH segment.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC   -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC       PATIENT WITH MACROGLOBULINEMIA.
DR   PIR; A02051; M3HUAM.
DR   HSSP; P01772; 2IG2.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13668 MW;  A42D0F17D252F1C2 CRC64;


  Query Match             52.0%;  Score 51;  DB 1;  Length 122;
  Best Local Similarity   66.7%;  Pred. No. 0.12;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       6 NKRAMDYWGQGT 17
           : || :||||||
Db     105 BYRAFNYWGQGT 116


RESULT   3
HV[illegible]OUSE
ID   HV42_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01812;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 1-104.
RX   MEDLINE=72105531; PubMed=5062012;
RA   Bourgois A., Fougereau M., de Preval C.;
RT   "Sequence of amino acids of the NH 2 -terminal region of a
RT   mouse-clonal immunoglobulin heavy chain.";
RL   Eur. J. Biochem. 24:446-455(1972).
RN   [2]
RP   SEQUENCE OF 105-117.
RX   MEDLINE=76091933; PubMed=812695;
RA   Rocca-Serra J., Milili M., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the H4 cyanogen-bromide
RT   fragment.";
RL   Eur. J. Biochem. 59:511-523(1975).
RN   [3]
RP   SEQUENCE OF 96-117 FROM N.A.
RX   MEDLINE=81223769; PubMed=6787590;
RA   Gough N.M., Bernard O.;
RT   "Sequences of the joining region genes for immunoglobulin heavy
RT   chains and their role in generation of antibody diversity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:509-513(1981).
RN   [4]
RP   DISULFIDE BOND.
RA   Bourgois A., Fougereau M.;
RT   "Partial amino acid sequence of the variable region of a mouse
RT   gammaG2a immunoglobulin heavy chain. Evidence for the existence of a
RT   third sub-group of variability for the heavy chain pool.";
RL   FEBS Lett. 8:265-268(1970).
CC   -!- MISCELLANEOUS: THIS GAMMA-2A CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN.
DR   PIR; A02082; G2MS73.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region.
FT   DISULFID     22     96
FT   CONFLICT    105    105       N -> D (IN REF. 2).
FT   NON_TER      117    117
SQ   SEQUENCE   117 AA;  13051 MW;  156DCCC259380F19 CRC64;


  Query Match             51.0%;  Score 50;  DB 1;  Length 117;
  Best Local Similarity   88.9%;  Pred. No. 0.16;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 AMDYWGQGT 17
           ||:||||||
Db     103 AMNYWGQGT 111


RESULT   4
HV07_MOUSE
ID   HV07_MOUSE     STANDARD;      PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A02034; MHMS18.
DR   InterPro; IPR003006; -.
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DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    139       IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DOMAIN      118    124       D SEGMENT.
FT   DOMAIN      125    139       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     139    139
SQ   SEQUENCE   139 AA;  15419 MW;  1B57DD4FD0C9F465 CRC64;


  Query Match             51.0%;  Score 50;  DB 1;  Length 139;
  Best Local Similarity   61.5%;  Pred. No. 0.19;
  Matches    8;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       5 YNKRAMDYWGQGT 17
           |     |||||||
Db     121 YGSSYFDYWGQGT 133


RESULT   5
HV15_MOUSE
ID   HV15_MOUSE     STANDARD;      PRT;   136 AA.
AC   P01759;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222262; PubMed=6806821;
RA   Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA   Blattner F.R.;
RT   "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT   by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT   by two adjacent CH genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC   -----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00494; AAA38130.1; -.
DR   PIR; A02042; HVMSB1.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    136       IG HEAVY CHAIN V REGION BCL1.
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15078 MW;  6827CFBC6DB3F35E CRC64;


  Query Match             50.0%;  Score 49;  DB 1;  Length 136;
  Best Local Similarity   57.1%;  Pred. No. 0.28;
  Matches    8;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       4 KYNKRAMDYWGQGT 17
           :|     |||||||
Db     117 RYYGNYFDYWGQGT 130


RESULT   6
HV11_MOUSE
ID   HV11_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00539; AAA38172.1; -.
DR   PIR; A02038; G2MS43.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    137       IG HEAVY CHAIN V REGION S43.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DOMAIN      118    122       D SEGMENT.
FT   DOMAIN      123    137       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     137    137
SQ   SEQUENCE   137 AA;  15200 MW;  ADD5881BF44B8EC9 CRC64;


  Query Match             50.0%;  Score 49;  DB 1;  Length 137;
  Best Local Similarity   80.0%;  Pred. No. 0.28;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       8 RAMDYWGQGT 17
           |  |||||||
Db     122 RYFDYWGQGT 131


RESULT   7
HV43_MOUSE
ID   HV43_MOUSE     STANDARD;      PRT;   144 AA.
AC   P01819;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81012133; PubMed=6774258;
RA   Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT   "Two types of somatic recombination are necessary for the generation
RT   of complete immunoglobulin heavy-chain genes.";
RL   Nature 286:676-683(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC       DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00491; AAA38121.1; -.
DR   EMBL; V00768; CAA24149.1; -.
DR   PIR; A02094; G2MS14.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    144       IG HEAVY CHAIN V REGION MOPC 141.
FT   NON_TER     144    144
SQ   SEQUENCE   144 AA;  15759 MW;  8E47A7CB3706D30A CRC64;


  Query Match             49.0%;  Score 48;  DB 1;  Length 144;
  Best Local Similarity   87.5%;  Pred. No. 0.43;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      10 MDYWGQGT 17
           :|||||||
Db     131 LDYWGQGT 138


RESULT   8
HV02_XENLA
ID   HV02_XENLA     STANDARD;      PRT;   135 AA.
AC   P20957;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION XIG14 PRECURSOR (FRAGMENT).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88176921; PubMed=2451244;
RA   Schwager J., Mikoryak C.A., Steiner L.A.;
RT   "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT   from cDNA sequence: implications for evolution of immunoglobulin
RT   domains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J03632; AAA49791.1; -.
DR   PIR; B31933; B31933.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     18
FT   CHAIN        19    135       IG HEAVY CHAIN V REGION XIG14.
FT   NON_TER     135    135
SQ   SEQUENCE   135 AA;  15080 MW;  EBC467105C00732E CRC64;


  Query Match             48.5%;  Score 47.5;  DB 1;  Length 135;
  Best Local Similarity   69.2%;  Pred. No. 0.49;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy       5 YNKRAMDYWGQGT 17
           ||    |||||||
Db     120 YN---FDYWGQGT 129


RESULT   9
HV35_MOUSE
ID   HV35_MOUSE     STANDARD;      PRT;   111 AA.
AC   P01804;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V-III REGION HPC76 (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81013937; PubMed=6251474;
RA   Bernard O., Gough N.M.;
RT   "Nucleotide sequence of immunoglobulin heavy chain joining segments
RT   between translocated VH and mu constant regions genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
CC       REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
CC       CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
DR   PIR; A02074; MHMS76.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region.
FT   NON_TER       1      1
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12304 MW;  0EDE98EC7348056A CRC64;


  Query Match             46.9%;  Score 46;  DB 1;  Length 111;
  Best Local Similarity   100.0%;  Pred. No. 0.7;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 DYWGQGT 17
           |||||||
Db      99 DYWGQGT 105


RESULT  10
HV3T_HUMAN
ID   HV3T_HUMAN     STANDARD;      PRT;   116 AA.
AC   P01781;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V-III REGION GAL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059123; PubMed=4803843;
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RA   Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT   type), subgroup H III. Architecture of the complete IgM-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN   [2]
RP   REVISION TO THE COMPOSITION OF 28-33.
RA   Hilschmann N.;
RL   Submitted (JUN-1975) to the PIR data bank.
CC   -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC       MACROGLOBULIN.
DR   PIR; A02064; M3HUGL.
DR   HSSP; P01772; 2IG2.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12730 MW;  2C67CA9AAAAA1282 CRC64;


  Query Match             46.9%;  Score 46;  DB 1;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 0.74;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 DYWGQGT 17
           |||||||
Db     104 DYWGQGT 110


RESULT  11
HV39_MOUSE
ID   HV39_MOUSE     STANDARD;      PRT;   118 AA.
AC   P01809;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION X24.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in
RT   complementarity-determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC       THAT BINDS GALACTAN.
DR   PIR; A02079; AVMSX2.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region.
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13105 MW;  BB16A2DB677EF17F CRC64;


  Query Match             46.9%;  Score 46;  DB 1;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 0.75;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 DYWGQGT 17
           |||||||
Db     105 DYWGQGT 111


RESULT  12
HV03_MOUSE
ID   HV03_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC       DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC       CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC       SEGMENT, JH2.
DR   PIR; A02028; HVMSG7.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13307 MW;  FF04E4A167B654AF CRC64;


  Query Match             46.9%;  Score 46;  DB 1;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 0.76;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 DYWGQGT 17
           |||||||
Db     108 DYWGQGT 114


RESULT  13
HV1H_HUMAN
ID   HV1H_HUMAN     STANDARD;      PRT;   120 AA.
AC   P80421;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V-I REGION DOT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region.
FT   DISULFID     22     95       BY SIMILARITY.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13272 MW;  F1307FD253A782F1 CRC64;


  Query Match             46.9%;  Score 46;  DB 1;  Length 120;
  Best Local Similarity   53.8%;  Pred. No. 0.76;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 YNKRAMDYWGQGT 17
           :::  || |||||
Db     102 FSQYGMDVWGQGT 114
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RESULT  14
HV3K_HUMAN
ID   HV3K_HUMAN     STANDARD;      PRT;   126 AA.
AC   P01772;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V-III REGION KOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=81072295; PubMed=7441755;
RA   Marquart M., Deisenhofer J., Huber R., Palm W.;
RT   "Crystallographic refinement and atomic models of the intact
RT   immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT   and 1.0-A resolution.";
RL   J. Mol. Biol. 141:369-391(1980).
DR   PIR; A02055; G1HUKL.
DR   PDB; 2FB4; 12-JUL-89.
DR   PDB; 2IG2; 12-JUL-89.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     96
FT   DISULFID    105    110
FT   STRAND        3      7
FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
FT   STRAND       46     51
FT   TURN         53     54
FT   STRAND       58     60
FT   TURN         62     67
FT   STRAND       68     73
FT   TURN         74     77
FT   STRAND       78     83
FT   HELIX        88     90
FT   STRAND       92     99
FT   STRAND      106    106
FT   TURN        107    108
FT   STRAND      109    109
FT   STRAND      113    113
FT   STRAND      120    124
FT   NON_TER     126    126
SQ   SEQUENCE   126 AA;  13718 MW;  E4D71B52B16F8776 CRC64;


  Query Match             46.9%;  Score 46;  DB 1;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 0.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 DYWGQGT 17
           |||||||
Db     114 DYWGQGT 120


RESULT  15
HV46_MOUSE
ID   HV46_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01822;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MOPC 315 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89238351; PubMed=2497341;
RA   Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT   "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT   gene segment.";
RL   Mol. Immunol. 26:431-434(1989).
RN   [2]
RP   SEQUENCE OF 1-31.
RX   MEDLINE=78094475; PubMed=414225;
RA   Jilka R.L., Pestka S.;
RT   "Amino acid sequence of the precursor region of MOPC-315 mouse
RT   immunoglobulin heavy chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN   [3]
RP   SEQUENCE OF 1-21.
RX   MEDLINE=79148758; PubMed=428562;
RA   Schechter I., Wolf O., Zemell R., Burstein Y.;
RT   "Structure and function of immunoglobulin genes and precursors.";
RL   Fed. Proc. 38:1839-1845(1979).
RN   [4]
RP   SEQUENCE OF 19-136.
RX   MEDLINE=74170779; PubMed=4524622;
RA   Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT   "Amino-acid sequence of the variable region of the heavy (alpha)
RT   chain of a mouse myeloma protein with anti-hapten activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN   [5]
RP   REVISION TO 53.
RX   MEDLINE=77244979; PubMed=268248;
RA   Hood L., Margolies M.N., Givol D., Zakut R.;
RL   Unpublished results, cited by:
RL   Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL   Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC   -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M27638; AAA61337.1; -.
DR   EMBL; X07880; CAA30727.1; -.
DR   PIR; PL0102; AVMS35.
DR   InterPro; IPR003006; -.
DR   Pfam; PF00047; ig; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    137       IG HEAVY CHAIN V REGION MOPC 315.
FT   DOMAIN       19     48       FRAMEWORK 1.
FT   DOMAIN       49     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     84       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       85    116       FRAMEWORK 3.
FT   DOMAIN      117    126       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      127    137       FRAMEWORK 4.
FT   DISULFID     40    114       BY SIMILARITY.
FT   CONFLICT     15     15       G -> GG (IN CAA30727).
FT   CONFLICT     15     15       G -> H (IN REF. 2).
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FT   CONFLICT     77     78       GY -> YG (IN REF. 4).
FT   CONFLICT    102    102       N -> D (IN REF. 4).
FT   CONFLICT    123    123       MISSING (IN REF. 4).
FT   NON_TER     137    137
SQ   SEQUENCE   137 AA;  15399 MW;  FB3828304C2B81DC CRC64;


  Query Match             46.9%;  Score 46;  DB 1;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 0.88;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 DYWGQGT 17
           |||||||
Db     125 DYWGQGT 131


Search completed: June 27, 2001, 11:33:21
Job time: 266 sec
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